



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/667,569

Source: CIPR

Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821-1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Run Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/667,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 ☐ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

- 8 ☐ Skipped Sequences Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s)

- 9 ☐ Skipped Sequences Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 10 ☒ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

- 11 ☐ Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence

- 12 ☐ Use of <220>Feature Sequence(s) ____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing)
Instead, please use "File Manager" or any other means to copy file to floppy disk

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/667,569

DATE: 05/07/2001
 TIME: 17:56:42

Input Set : A:\sequence.txt
 Output Set: N:\CRF3\05072001\I667569.raw

3 <110> APPLICANT: Yocum, R. et al.
 5 <120> TITLE OF INVENTION: METHODS AND MICROORGANISMS FOR PRODUCTION OF
 6 PANTO-COMPOUNDS
 8 <130> FILE REFERENCE: BGI-141CP
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/667,569
 C--> 11 <141> CURRENT FILING DATE: 2000-09-21
 13 <150> PRIOR APPLICATION NUMBER: USSN 09/400,494
 14 <151> PRIOR FILING DATE: 1999-09-21
 16 <150> PRIOR APPLICATION NUMBER: USSN 60/210,072
 17 <151> PRIOR FILING DATE: 2000-06-07
 19 <150> PRIOR APPLICATION NUMBER: USSN 60/221,836
 20 <151> PRIOR FILING DATE: 2000-07-28
 W--> 22 <150> PRIOR APPLICATION NO: USSN 60/221,836 *I - Duplicate application number.*
 23 <151> PRIOR FILING DATE: 2000-08-24
 25 <160> NUMBER OF SEQ ID NOS: 94
 27 <170> SOFTWARE: PatentIn Ver. 2.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 311
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Haemophilus influenzae
 34 <400> SEQUENCE: 1
 35 Met Glu Phe Ser Thr Gln Gln Thr Pro Phe Leu Ser Phe Asn Arg Glu
 36 1 5 10 15
 38 Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln
 39 20 25 30
 41 Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu
 42 35 40 45
 44 Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile
 45 50 55 60
 47 Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg
 48 65 70 75 80
 50 Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala
 51 85 90 95
 53 Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His
 54 100 105 110
 56 Trp Pro Thr Glu Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu
 57 115 120 125
 59 Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
 60 130 135 140
 62 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 63 145 150 155 160
 65 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 66 165 170 175
 68 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 69 180 185 190
 71 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 72 195 200 205

Does Not Comply
 Corrected Diskette Needed
 pp. 1, 6

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,569

DATE: 05/07/2001

TIME: 17:56:42

Input Set : A:\sequence.txt

Output Set N:\CRF3\05072001\I667569.raw

```

74 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
75      210                      215                      220
77 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
78 225      230                      235                      240
80 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
81      245                      250                      255
83 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
84      260                      265                      270
86 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
87      275                      280                      285
89 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
90      290                      295                      300
92 Glu Leu Ile Lys Leu Arg Lys
93 305                      310
96 <210> SEQ ID NO 2
97 <211> LENGTH 316
98 <212> TYPE: PRT
99 <213> ORGANISM Escherichia coli
101 <400> SEQUENCE 2
102 Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp
103 1      5                      10                      15
105 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
106      20                      25                      30
108 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
109      35                      40                      45
111 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
112      50                      55                      60
114 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu
115 65      70                      75                      80
117 Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
118      85                      90                      95
120 Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
121      100                     105                     110
123 Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
124      115                     120                     125
126 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
127      130                     135                     140
129 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
130 145      150                     155                     160
132 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
133      165                     170                     175
135 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
136      180                     185                     190
138 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
139      195                     200                     205
141 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
142      210                     215                     220
144 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
145 225      230                     235                     240

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Input Set : A:\sequence.txt

Output Set: N:\CRF3\05072001\I667569.raw

```

147 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
148           245           250           255
150 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
151           260           265           270
153 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
154           275           280           285
156 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
157           290           295           300
159 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
160 305           310           315
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 319
165 <212> TYPE: PRT
166 <213> ORGANISM: Bacillus subtilis
168 <400> SEQUENCE 3
169 Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
170 1 5 10 15
172 Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
173 20 25 30
175 Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
176 35 40 45
178 Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
179 50 55 60
181 His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
182 65 70 75 80
184 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
185 85 90 95
187 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
188 100 105 110
190 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
191 115 120 125
193 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
194 130 135 140
196 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
197 145 150 155 160
199 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
200 165 170 175
202 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
203 180 185 190
205 Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
206 195 200 205
208 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
209 210 215 220
211 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
212 225 230 235 240
214 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
215 245 250 255
217 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
218 260 265 270

```

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Input Set : A:\sequence.txt

Output Set: N:\CRF3\05072001\I667569.raw

```

220 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
221           275           280           285
223 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
224           290           295           300
226 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
227 305           310           315
230 <210> SEQ ID NO: 4
231 <211> LENGTH: 312
232 <212> TYPE: PRT
233 <213> ORGANISM: Mycobacterium leprae
235 <400> SEQUENCE: 4
236 Met Pro Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Lys
237   1           5           10           15
239 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
240           20           25           30
242 Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
243           35           40           45
245 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
246           50           55           60
248 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
249   65           70           75           80
251 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
252           85           90           95
254 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
255           100          105          110
257 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
258           115          120          125
260 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
261           130          135          140
263 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
264 145           150          155          160
266 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
267           165          170          175
269 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
270           180          185          190
272 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
273           195          200          205
275 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
276           210          215          220
278 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
279 225           230          235          240
281 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
282           245          250          255
284 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
285           260          265          270
287 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
288           275          280          285
290 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
291           290          295          300

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/667,569

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 TIME: 17:56:42

Input Set A:\sequence.txt
 Output Set N:\CRF3\05072001\I667569.raw

```

293 Asn Arg Leu Arg Leu Arg Lys Leu
294 305 310
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 312
299 <212> TYPE: PRT
300 <213> ORGANISM: Mycobacterium tuberculosis
302 <400> SEQUENCE: 5
303 Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
304 1 5 10 15
306 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
307 20 25 30
309 Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
310 35 40 45
312 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
313 50 55 60
315 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
316 65 70 75 80
318 Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
319 85 90 95
321 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
322 100 105 110
324 Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
325 115 120 125
327 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
328 130 135 140
330 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
331 145 150 155 160
333 Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
334 165 170 175
336 Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
337 180 185 190
339 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
340 195 200 205
342 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
343 210 215 220
345 Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
346 225 230 235 240
348 Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
349 245 250 255
351 Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile
352 260 265 270
354 Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
355 275 280 285
357 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
358 290 295 300
360 Asn Arg Leu Arg Leu Arg Lys Leu
361 305 310
364 <210> SEQ ID NO: 6
365 <211> LENGTH 329

```

<210> (45)
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome
 binding site

<400> 45
 ttaagaaagg aggtgannnn atg 23

<210> (45)
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome
 binding site

<400> 45
 ttagaaagga ggtgannnnn atg 23

<210> (47)
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome
 binding site

<400> 47
 agaaagaggg tgannnnnnn atg 23

<210> (48)
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome
 binding site

<400> 48
 agaaagaggg tgannnnnna tg 23

* Some sequences are missing the mandatory
 <220> + <223> to allow to explain the "N's" in
 the sequences. See #10 on the Ecm.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/667,569

DATE 05/07/2001

TIME 17:56:43

Input Set : A:\sequence.txt

Output Set: N:\CRF3\05072001\I667569.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:288 W: Application Number is Repeated, <150> PRIOR APPLICATION NUMBER
L:2892 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2892 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2904 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2904 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2918 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47
L:2918 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:2918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:2930 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:2930 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:7767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88
L:7767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88
L:7767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88